

FIG. 1



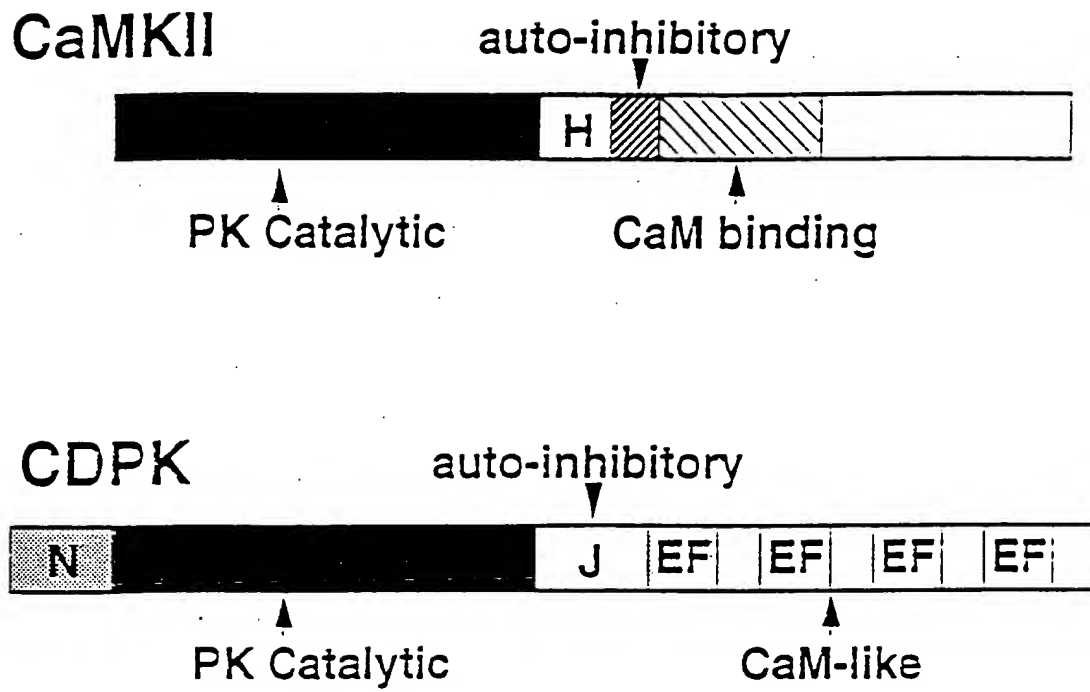


FIG. 3A

Atcdpk	HGHTCVGPR	NGFLQSVSA	MWRPRDGD	ASHNGDIA	EAVSGEIRSR	LSDEVQHKPP	60
Atcdpk1							0
Atcdpk1a							0
Atcdpk2							0
Atcdpk	EQVTTPKPGT	DVETKDRER	TESKPELEE	ISLESKPEK	QETKSETKPE	SKPDPAPKPK	120
Atcdpk1							0
Atcdpk1a							0
Atcdpk2							9
Atcdpk	KPKHHRVSS	AGLRTESVLQ	RKTEHFF	VS	QF	KT	179
Atcdpk1							40
Atcdpk1a							40
Atcdpk2							55
Atcdpk	SA	EP	Q	N	P	C	239
Atcdpk1							100
Atcdpk1a							100
Atcdpk2							115
Atcdpk	TV	KA	EV	V	F	L	299
Atcdpk1							160
Atcdpk1a							160
Atcdpk2							175
Atcdpk	VP	EA	EV	EA	EV	EA	359
Atcdpk1							220
Atcdpk1a							220
Atcdpk2							235
Atcdpk	EQV	HA	RA	RA	RA	RA	VDGVA11
Atcdpk1							HA KK271
Atcdpk1a							HA KK271
Atcdpk2							DEQA209

FIG. 3B

# PK Constructs

		1 a.a. ATG	413 a.a.	TGA
1.	35SC4PPDK	ATCDPK (AK1)	DHA	NOS
		274 a.a.		
2.	35SC4PPDK	ATCDPK1	DHA	NOS
		274 a.a.		
3.	35SC4PPDK	ATCDPK1a	DHA	NOS
		289 a.a.		
4.	35SC4PPDK	ATCDPK2	DHA	NOS
		284 a.a.		
5.	35SC4PPDK	ATPKa	DHA	NOS
		283 a.a.		
6.	35SC4PPDK	ATPKb	DHA	NOS
		265 a.a.		
7.	35SC4PPDK	ASK1	DHA	NOS
		265 a.a.		
8.	35SC4PPDK	ASK2	DHA	NOS

FIG. 3C

262T2T-18368680

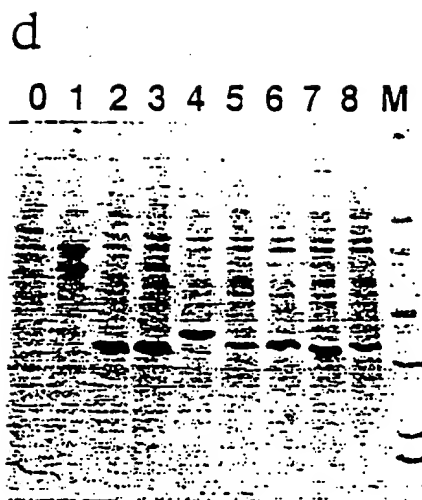


FIG. 3D

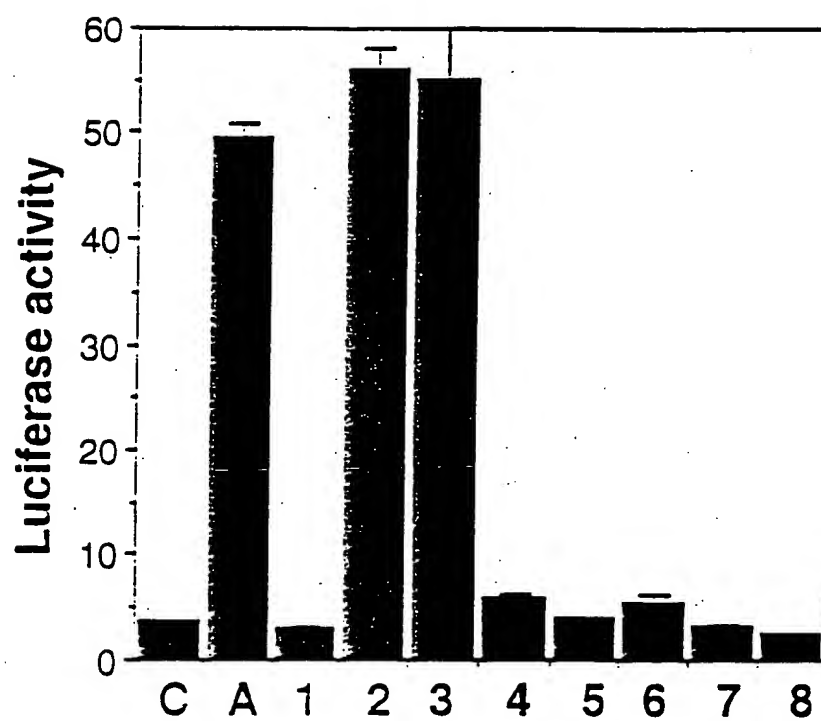
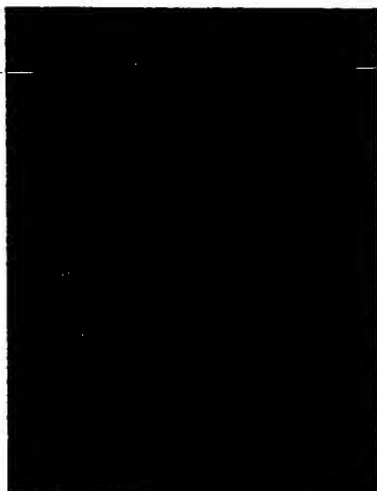


FIG. 3E



FIG. 4A

Control



CDPK1



CDPK1mut



FIG. 4B



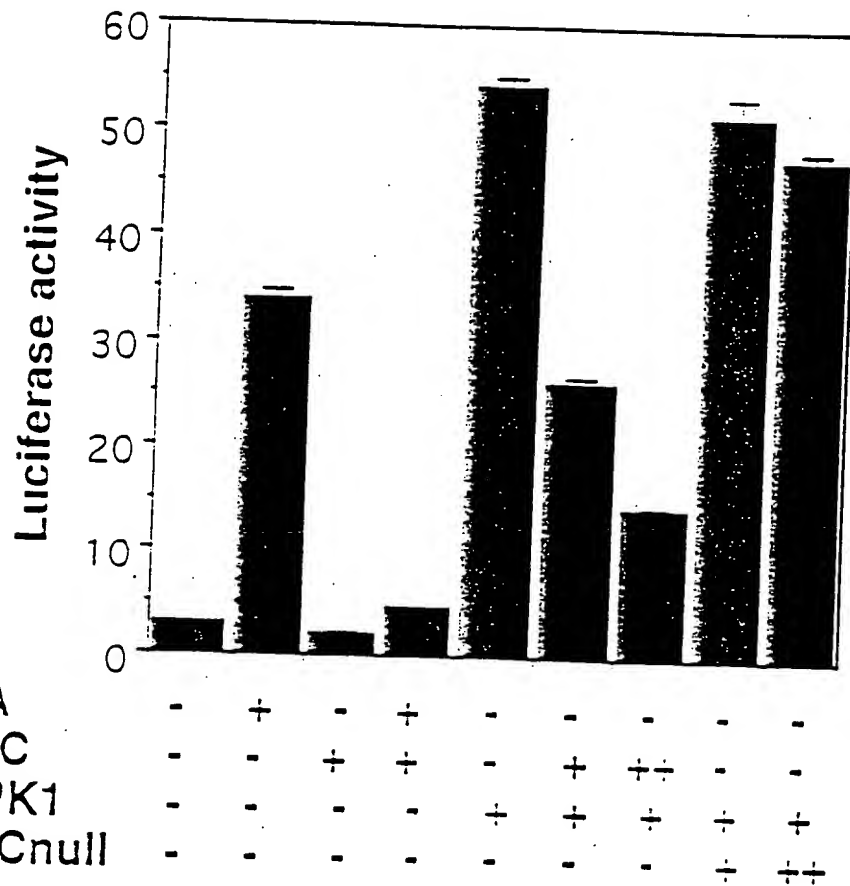


FIG. 4C

## A model of stress signalling in plant cells

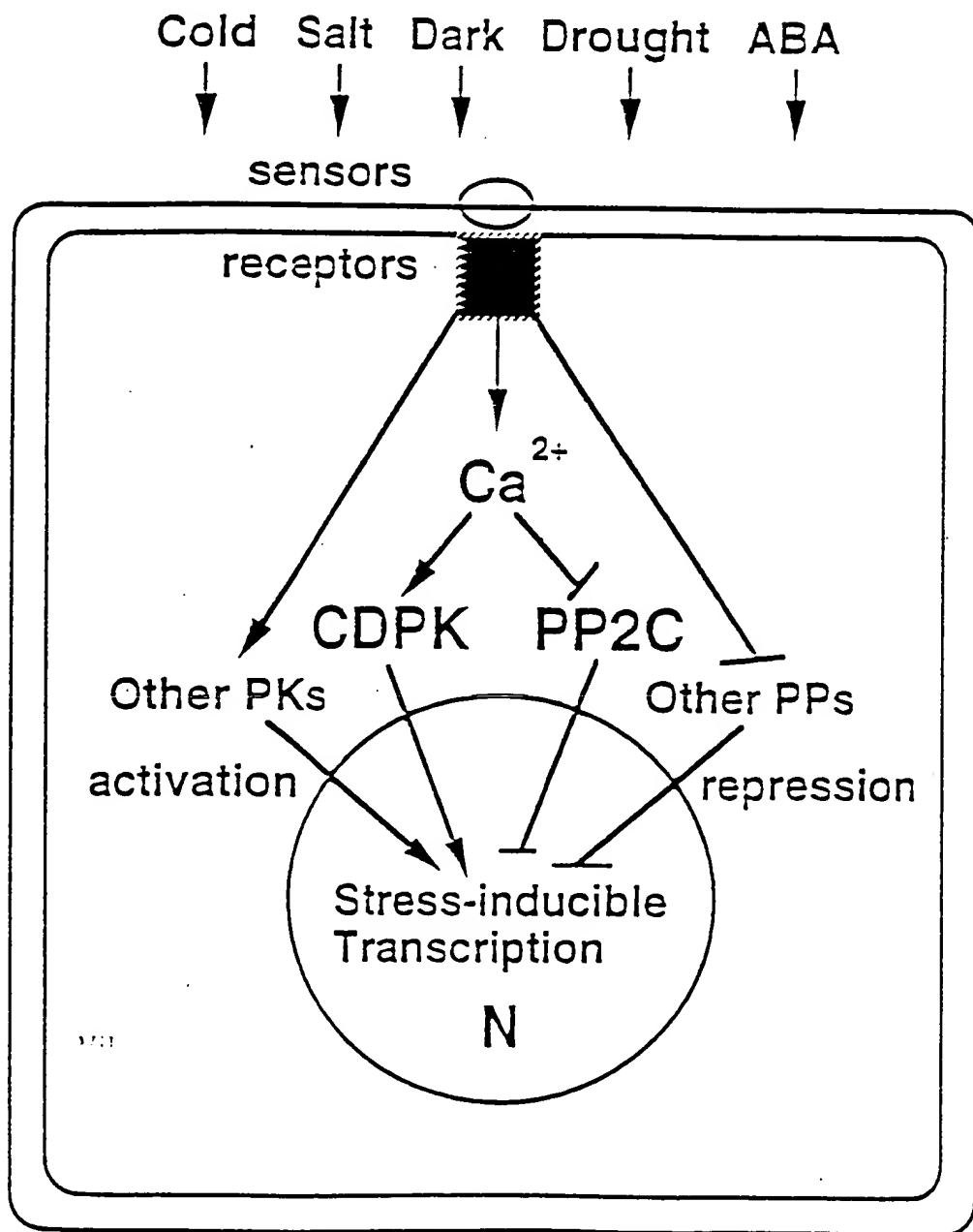


FIG. 4D

SEQ ID NO: 1  
1 GTTGTAAACGACGGNCAGTGAATTGTAATACGACTCNCATAGGGCGNAATTGGAGCTC  
-----+-----+-----+-----+-----+-----+ 60  
CAACATTTTCTGCGGCTCACTTAAACATTATGCTGAGNGATATCCCGCNTTAACCTCGAG

३

61 CACCGCGGTGGCGCGCGCTCTAGAACTAGTGGATCCATGGCTAATCAAACTCAGATCAGC 120  
-----+-----+-----+-----+  
GTGGCGCCACCGCGCGCGAGATCTTGATCACCTAGGTACCGATTAGTTTGAAGTCTAGTCG

SEQ ID NO: 2 → M A N Q T Q I S -

121 GACAAGTACATCTT<sup>+</sup>AGGACGAGA<sup>+</sup>ACTCGGTCCGGCGGAATTCGGAATC<sup>+</sup>ACGTATCTTTGT<sup>+</sup> 180

CTGTTTCATGTAGAANTCTGCTCTTTGAGCCAGCCCGCTTAAGCCTTAGTG<sup>+</sup>CATAGAACA<sup>+</sup>

a D K Y I L G R E L G R G E F G I T Y L C -

ACAGATAGAGAGACTCGTGAAGCTTTAGCTTGCAAATCAATCTCCAAGAGAAAGGCTCGGA  
-----+-----+-----+-----+-----+-----+-----+  
181 TGTCTATCTCTCGAGCACTTCGAAATCGAACGTTTAGTTAGAGGTTCTCTTTCGAGGCT 240  
  
T D R E T R E A L A C K S I S K R K L R -

241 ACCGCCGTCGATGTGGAAGACGTCGTCGTGAAGTCACGATCATGTCTAACTTTACCGGAA 300  
-----+-----+-----+-----+-----+-----+-----+  
TGGCGGCAGCTACACCTTCTGCAGGCAGCACTTCAGTGCTAGTACAGTTGAAATGGCCTT  
  
T A V D V E D V R R E V T I M S T L P E -

301 CACCCAAACGTTGTGAAACTTTAAGCGACTTATGAGGATAACGAGACCGTGCATCTTTGTG 360  
 -----+-----+-----+-----+-----+-----+-----+-----  
 GTGGGTTTGCAACACTTTGAATTCGCTGAATACTCCTATTGCTCTGGCACGTAGAACAC  
 - H P N V V K L K A T Y E D N E T V H L V -

361 ATGGAGCTTTGTGAAGGAGGTGAGCTTTTGGTCGGATTGTTGCAAGAGGACATTATACA 420  
-----+-----+-----+-----+-----+-----+  
TACCTCGAAACACTTCCTCCACTCGAAAAACCAGCCTAACACGTTCTCCTGTAATATGT  
M E L C E G G E L F G R I V A R G H Y T -

421 GAGCGTGGCGGGCTACCGTCGCGAGAACGATCGCGGAAGTTGTGAGGATGTGTCAATGTC 480  
-----+-----+-----+-----+-----+  
CTCGCACGCGCGCGGATGGCAGCGCTCTTGCTAGCGCCTTCAACACTCCTACACAGTACAG  
E R A A A T V A R T I A E V V R M C H V -

FIGURE 5 (SHEET 3/4)

AATGGTGTATGCATAGAGATTGGAAGCCTGAGAATTTCTTGTGCTAACAAGRAGGAG  
 481 -----+-----+-----+-----+-----+ 540  
 TTACCACAATACGTATCTCTAAACTTCGGACTCTTAAAGAACAACGATTGTTCTTCCTC

a , N G V M H R D L K P E N F L F A N K K E -

AATTCTGCACCTTAAGGCTATTGATTTTGGTTTATCTGTCTCTTTAAACCTGGAGAGAGG  
 541 -----+-----+-----+-----+-----+ 600  
 TTAAGACGTGAATTCGGATAACTAAAACCAAATAGACAAGAGAAATTTGGACCTCTCTCC

a N S A L K A I D F G L S V L F K P G E R -

TTTACAGAGATTGTTGGAAGTCCTTATTATATGGCTCCAGAAGTGTGGAAGAGAAATTAT  
 601 -----+-----+-----+-----+-----+ 660  
 AAATGTCTCTAACACCTTCAGGAATAATATACCGAGGTCTTCACAACCTTCTTTAATA

a F T E I V G S P Y Y M A P E V L K R N Y -

GGACCAGAGGTTGATGTGTGGAGTGGCTGGAGTTATCCTCTACATCTTGCTTTGTGGTGT  
 661 -----+-----+-----+-----+-----+ 720  
 CCTGGTCTCCAACCTACACACCTCACGACCTCAATAGGAGATGTAGAACGAAACACCAAA

a G P E V D V W S A G V I L Y I L L C G V -

0099991-12197

FIGURE 5 (SHEET 4/4)

721 CCTCCGTTTTGGGCAGAGACTGAACAAGGTGTGGCTCTTGCCATCTGAGGGGAGTTCTT  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 780  
 GGAGGCCAAACCCCTCTCTGACTTGTTCACACCGAGAACGGTAGAACTCCCTCAAGAA  
 P P F W A E T E Q G V A L A I L R G V L -

781 GATTTTAAGAGAGATCCTTGGTCGCAGATATCAGAGAGCGCAAAGAGCCTTGTGAAGCAG  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840  
 CTAAAATTCTCTCTAGGAACCAGCGTCTATAGTCTCTCGCGTTTCTCGGAACACTTCGTC  
 D F K R D P W S Q I S E S A K S L V K Q -

841 ATGTTGGAACCTGATTCAACTAAGCGTTTGACTGCTCAGCAAGTTCTTGATCACCCTTGG  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900  
 TACAACCTTGGACTAAGTTGATTGCGAAACTGACGAGTCGTTCAAGAACTAGTGGGAACC  
 M L E P D S T K R L T A Q Q V L D H P W -

901 ATACAGAATGCAAAGAAAGGATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960  
 TATGTCTTACGTTTCTTTTCCTAGTTGGAATAGCTATGGCAGCTGGAGCTCCCCCGGG  
 I Q N A K K

17/1

961 GGTACCAGCTTTNGTTCCCTTTAGTGAGGGTTAATTTGAGCTTGGCGTAATCATGTCAT  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
 CCATCGTGGAAANCAAGGGAAATCACTCCCAATTAAAGCTCGAACCGCATTAGTACAGTA

L62T2T" T888880